



SEQUENCE LISTING

<110> Turck, Jutta
Archer, John

<120> CONTROL OF GENE EXPRESSION IN EUKARYOTES

<130> 13101/48202

<140> US 10/732,859

<141> 2003-12-09

<150> UK 9828660.2

<151> 1998-12-24

<150> US 09/469,211

<151> 1999-12-22

<160> 19

<170> PatentIn version 3.3

<210> 1

<211> 7599

<212> DNA

<213> Rhodococcus sp.

<220>

<221> CDS

<222> (295)..(1035)

<220>

<221> CDS

<222> (1261)..(2805)

<220>

<221> CDS

<222> (2807)..(4720)

<220>

<221> CDS

<222> (5721)..(6665)

<400> 1

gaattccatg ttcttctcct tgcgttgcc ccgcgttgcc gagggcactg ctcggcctgt 60

cgcggcgaga gggcgcatgt ccgggtgcct ggatatggcg cgtacggcgt gcccctccggc 120

gttaaccccg aggttggcca cgatgccccg gccatcaggt ctgaaatgct agcgttccag 180

acgaaggtaa cccacagtga ctcacaccac aagtactaga atgcaagctg ttgcggtag 240

cggccggca taagggggag ccatgtccgg gacgccgacg gaaagcctga ctcg atg 297

Met

1

acc acc acc gac acc ggc ccc aag ccg ggc agt gag gcc gcc gcc ctg Thr Thr Thr Asp Thr Gly Pro Lys Pro Gly Ser Glu Ala Ala Ala Leu	5	10	15	345	
ctc gcc aat gtc cgc acc tcg ggg gcg cggttgc tcc tcc gcg ttgtac Leu Ala Asn Val Arg Thr Ser Gly Ala Arg Leu Ser Ser Ala Leu Tyr	20	25	30	393	
gac att ctg aag aac cgg ctg ctc gaa ggg cgc tat gcg gca ggc gag Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg Tyr Ala Ala Gly Glu	35	40	45	441	
aag atc gtc gtc gag tcg atc cgg caa gag ttc ggg gtgtac gac aag cag Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe Gly Val Ser Lys Gln	50	55	60	65	489
ccc gtc atg gac gct ctg cgc ctg tcc agc gac aag ctg gtc cac Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser Asp Lys Leu Val His	70	75	80	537	
atc gtt ccc cag gtc ggt tgc gag gtc gtc tcc tac gcc ccg cgc gaa Ile Val Pro Gln Val Gly Cys Glu Val Val Ser Tyr Ala Pro Arg Glu	85	90	95	585	
gtg gaa gac ttc tac acc ctg ttc ggc ggt ttc gaa ggg acc atc gcc Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe Glu Gly Thr Ile Ala	100	105	110	633	
gcg gta gcg gcc tcc cgg cgg acc gag gcc cag ttgtac gac aac atc Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln Leu Leu Glu Leu Asp	115	120	125	681	
ctg atc tcg gcg cgg gtc gac gcc ctg atc acc tcc cac gac ccg gtg Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp Pro Val	130	135	140	145	729
gtc cgc gcc cgc ggg tac cgc gtgtac cac aac cgg gag ttc cat gcg gcc Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His Ala Ala	150	155	160	777	
atc cac gcg atg gcg cac tcg cgg atc atg gag gag acc agc cag cga Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser Gln Arg	165	170	175	825	
atg tgg gat ctg tcg gac ttc ttgtac aac acc acc ggc atc acc aac Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile Thr Asn	180	185	190	873	
ccg ctc tcg agc gca ctg ccc gac cgg cag cat gac cac cac gaa atc Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His Glu Ile	195	200	205	921	
acc gag gcc atc cgc aac cgt gac gca gct gcc gcc cgc gag gcc atg Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Ala Arg Glu Ala Met	210	215	220	225	969

gaa cgc cac atc gtc ggc acc atc gca gta atc cgc gac gaa tcc aac		1017	
Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser Asn			
230	235	240	
 gcc cag ctg ccg agc tag accccgatac ccggggccatc gaccggctcc		1065	
Ala Gln Leu Pro Ser			
245			
 gctatcgccc cacctacgccc gaggggggac tctcgccgt agcgctgcag acgatccacc		1125	
ggcacccctcc acgctgaccc ctgtctcgcc ctagaggccc ggccgcgcgt cgatcacctt		1185	
taccctcatc cagagacttg cgtcaccctc tatgcccag tagcgtctga actagacgtc		1245	
tagcattcta gttga gtg ctc ctc gaa gat tct cca gag aac ccc tct		1296	
Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser			
250	255		
 cga aca tcc cca gaa gaa agg agc ggc cat gac gac cgc ttc gca cgc		1344	
Arg Thr Ser Pro Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg			
260	265	270	
 atc gtc ctt cgg ggc acg agc cca ctt ccg ccc aca gat cgg gga agc		1392	
Ile Val Leu Arg Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser			
275	280	285	290
 ccg acc gtg agc acc aca cct acc tcc ccg acg aag acc tca ccg ctg		1440	
Pro Thr Val Ser Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu			
295	300	305	
 ccg gta gcg atg gcc agc ttc atc ggt acc acc gtc gag tac tac gac		1488	
Arg Val Ala Met Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp			
310	315	320	
 ttc ttc atc tac ggc acc gcg gcc gcg ctg gta ttc cct gag ttg ttc		1536	
Phe Phe Ile Tyr Gly Thr Ala Ala Leu Val Phe Pro Glu Leu Phe			
325	330	335	
 ttc ccg gat gtc tcg tcc gcg atc gga atc ctg ttg tcg ttc gcg acc		1584	
Phe Pro Asp Val Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr			
340	345	350	
 ttc agc gtt ggg ttc ctc gcc cgc ccg ctg ggt ggc ata gtg ttc ggg		1632	
Phe Ser Val Gly Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly			
355	360	365	370
 cac ttc ggt gac cgg gtc ggc cgc aag cag atg ctg gtg atc tcc ctg		1680	
His Phe Gly Asp Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu			
375	380	385	
 gtc gga atg ggc tcg gcc acc gta ctg atg gga ttg ttg ccc ggt tac		1728	
Val Gly Met Gly Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr			
390	395	400	

gcc caa atc ggg atc gcc ccc atc ctg ctg acc ctg ctg cgcc Ala Gln Ile Gly Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu	405	410	415	1776	
gtg cag ggc ttt gcc gtc ggc ggc gag tgg ggt gga gcc acc ctg atg Val Gln Gly Phe Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met	420	425	430	1824	
gcc gtc gag cac gcc ccc acc gcg aag aag ggc ttt ttc gga tcc ttc Ala Val Glu His Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe	435	440	445	1872	
tcc cag atg ggg gca ccc gcc ggg acc agc gtc gca acc ctg gcg ttc Ser Gln Met Gly Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe	455	460	465	1920	
ttc gcg gtc tcc caa ttg ccc gac gag cag ttc ctg agt tgg ggc tgg Phe Ala Val Ser Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp	470	475	480	1968	
cga ctg ccg ttc ctg ttc agc gcg gtg ctg atc gtg atc ggg ctg ttc Arg Leu Pro Phe Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe	485	490	495	2016	
att cgc ctg tcc ctg gcc gaa agc ccc gac ttc gcc gag gtg aag gca Ile Arg Leu Ser Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala	500	505	510	2064	
cag agc gcc gtg gtg cga atg ccg atc gcc gaa gcg ttc cgc aag cac Gln Ser Ala Val Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His	515	520	525	530	2112
tgg aag gaa att ctc ctc atc gcg ggc acc tac ctg tcc caa gga gtg Trp Lys Glu Ile Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val	535	540	545	2160	
ttc gcc tat atc tgc atg gcc tac ctc gtc tcc tac ggc acc acc gtc Phe Ala Tyr Ile Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val	550	555	560	2208	
gcg ggg atc agc cgc acc ttc gcc ctg gcc gga gta ttc gtc gcc ggc Ala Gly Ile Ser Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly	565	570	575	2256	
atc gtc gcc gtc ctc tac ctc gtg ttc ggc gct ctg tcc gac act Ile Val Ala Val Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr	580	585	590	2304	
ttc ggc cgc aag acc atg tac ctc gtc ggc gcc gcc gcg atg ggt gtg Phe Gly Arg Lys Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val	595	600	605	610	2352
gtg atc gcc ccc gcc ttc gca ctg atc aac acc ggc aac ccg tgg ctg Val Ile Ala Pro Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu	615	620	625	2400	

ttc atg gcc gcg cag gtg ctg gtc ttc gga att gca atg gcc ccc gcc Phe Met Ala Ala Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala	630	635	640	2448	
gcc ggc gtg aca ggc tcc ctg ttc acg atg gtc ttc gac gcg gac gtg Ala Gly Val Thr Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val	645	650	655	2496	
cgc tac agc ggt gtc tct atc ggc tac acc atc tcc cag gtc gcc ggc Arg Tyr Ser Gly Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly	660	665	670	2544	
tcc gcg ttc gcc ccg acg atc gcg acc gcc ttg tac gcc tcc acc aac Ser Ala Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn	675	680	685	690	2592
acc agc aac tcg atc gtg acc tac ctg ctg atc gtc tcg gcc atc tcg Thr Ser Asn Ser Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser	695	700	705	2640	
atc gtc tcg gtg atc ctg ctg ccc ggc ggc tgg ggg cgc aag ggc gct Ile Val Ser Val Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala	710	715	720	2688	
gcg agc cag ctc act cgc gac cag gcc acc tcc aca ccg aaa atg cct Ala Ser Gln Leu Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro	725	730	735	2736	
gac acc gaa aca ttt tcg act cg ^g aca gtt ccg gac acc gca gca tcc Asp Thr Glu Thr Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser	740	745	750	2784	
ctg cgc gtc ctc gac aag tga a gtg atg aca gac atg agt gac cac gac Leu Arg Val Leu Asp Lys Val Met Thr Asp Met Ser Asp His Asp	755	760	765	2833	
cgc acc tcc tac gac acc gac gtc gtg atc gtc ggc ctc ggc ccc gcc Arg Thr Ser Tyr Asp Thr Asp Val Val Ile Val Gly Leu Gly Pro Ala	770	775	780	785	2881
ggt ggc aca gcg gcg ctt gcc ctg gcc agc tac ggc atc cgc gtt cac Gly Gly Thr Ala Ala Leu Ala Leu Ala Ser Tyr Gly Ile Arg Val His	790	795	800	2929	
gcc gtc tcg atg ttc ccc tgg gtg gcg aac tcg ccg cgc gcg cac atc Ala Val Ser Met Phe Pro Trp Val Ala Asn Ser Pro Arg Ala His Ile	805	810	815	2977	
acc aac cag cgc gcc gtc gaa gtg ctg cgt gac ctg ggc gtc gaa gac Thr Asn Gln Arg Ala Val Glu Val Leu Arg Asp Leu Gly Val Glu Asp	820	825	830	3025	
gag gcg cgc aac tac gcc acc ccg tgg gac cag atg ggc gac acg ctg Glu Ala Arg Asn Tyr Ala Thr Pro Trp Asp Gln Met Gly Asp Thr Leu	835	840	845	3073	

ttc acc acg agc ctg gcc ggc gag gag atc gtc cgg atg cag acc tgg Phe Thr Thr Ser Leu Ala Gly Glu Glu Ile Val Arg Met Gln Thr Trp 850 855 860 865	3121
ggt acg ggc gat atc cgc tac ggg gac tac ctg tcc gga agc ccc tgc Gly Thr Gly Asp Ile Arg Tyr Gly Asp Tyr Leu Ser Gly Ser Pro Cys 870 875 880	3169
acg atg ctc gac att ccg cag ccc ctg atg gag ccg gtg ctg atc aag Thr Met Leu Asp Ile Pro Gln Pro Leu Met Glu Pro Val Leu Ile Lys 885 890 895	3217
aac gcc gcc gaa cgt ggt gcg gtc atc agc ttc aac acc gaa tac ctc Asn Ala Ala Glu Arg Gly Ala Val Ile Ser Phe Asn Thr Glu Tyr Leu 900 905 910	3265
gac cac gcc cag gac gag ggg gtg acc gtc cgg ttc cgc gac gtc Asp His Ala Gln Asp Glu Asp Gly Val Thr Val Arg Phe Arg Asp Val 915 920 925	3313
cgc tcg ggc acc gtg ttc acc cag cga gcc cgc ttc ctg ctc ggt ttc Arg Ser Gly Thr Val Phe Thr Gln Arg Ala Arg Phe Leu Leu Gly Phe 930 935 940 945	3361
gac ggc gca cga tcg aag atc gcc gaa cag atc ggg ctt ccg ttc gaa Asp Gly Ala Arg Ser Lys Ile Ala Glu Gln Ile Gly Leu Pro Phe Glu 950 955 960	3409
ggt gaa ctc gcc cgc gcc ggt acc gcg tac atc ctg ttc aac gcg gac Gly Glu Leu Ala Arg Ala Gly Thr Ala Tyr Ile Leu Phe Asn Ala Asp 965 970 975	3457
ctg agc aaa tat gtc gct cat cgg ccg agc atc ttg cac tgg atc gtc Leu Ser Lys Tyr Val Ala His Arg Pro Ser Ile Leu His Trp Ile Val 980 985 990	3505
aac tcg aag gcc ggt ttc ggt gag atc ggc atg ggt ctg ctg cgc gcg Asn Ser Lys Ala Gly Phe Gly Glu Ile Gly Met Gly Leu Leu Arg Ala 995 1000 1005	3553
atc cga ccg tgg gac cag tgg atc gcc ggc tgg ggc ttc gac atg Ile Arg Pro Trp Asp Gln Trp Ile Ala Gly Trp Gly Phe Asp Met 1010 1015 1020	3598
gcg aac ggc gag ccg gat gtc tcc gac gac gtt gtc ctc gaa cag Ala Asn Gly Glu Pro Asp Val Ser Asp Asp Val Val Leu Glu Gln 1025 1030 1035	3643
atc cgg acc ctc gtc ggc gac ccg cac ctg gac gtc gag atc gtg Ile Arg Thr Leu Val Gly Asp Pro His Leu Asp Val Glu Ile Val 1040 1045 1050	3688
tcg agg tcc ttc tgg tac gtc aac ccg cag tgg gct gag cac tac Ser Arg Ser Phe Trp Tyr Val Asn Arg Gln Trp Ala Glu His Tyr 1055 1060 1065	3733

cag	tcc	ggt	cga	gtg	ttc	tgc	ggc	ggc	gac	gcg	gtg	cac	cgg	cat		3778
Gln	Ser	Gly	Arg	Val	Phe	Cys	Gly	Gly	Asp	Ala	Val	His	Arg	His		
1070				1075						1080						
ccg	ccg	agc	agc	ggg	ctg	ggc	tcg	aac	acg	tcc	atg	cag	gac	gcg		3823
Pro	Pro	Ser	Ser	Gly	Leu	Gly	Ser	Asn	Thr	Ser	Met	Gln	Asp	Ala		
1085				1090						1095						
ttc	aat	ctg	gca	tgg	aag	atc	gcg	ttc	gtc	gtg	aag	ggg	tat	gca		3868
Phe	Asn	Leu	Ala	Trp	Lys	Ile	Ala	Phe	Val	Val	Lys	Gly	Tyr	Ala		
1100					1105					1110						
gga	ccg	ggt	ctg	ctc	gag	tcc	tac	tct	cct	gag	cgt	gtt	ccg	gtc		3913
Gly	Pro	Gly	Leu	Leu	Glu	Ser	Tyr	Ser	Pro	Glu	Arg	Val	Pro	Val		
1115					1120					1125						
ggc	aaa	cag	atc	gtc	gct	cgc	gcc	aac	cag	tcc	cgc	aag	gac	tac		3958
Gly	Lys	Gln	Ile	Val	Ala	Arg	Ala	Asn	Gln	Ser	Arg	Lys	Asp	Tyr		
1130					1135					1140						
gcc	ggg	ctg	cgc	gaa	tgg	ttc	gat	cac	gag	agc	gac	gac	ccg	gtc		4003
Ala	Gly	Leu	Arg	Glu	Trp	Phe	Asp	His	Glu	Ser	Asp	Asp	Pro	Val		
1145					1150					1155						
gcc	gcc	ggc	ctg	gca	aag	ttg	aag	gaa	ccc	tcg	tcc	gaa	ggt	gtt		4048
Ala	Ala	Gly	Leu	Ala	Lys	Leu	Lys	Glu	Pro	Ser	Ser	Glu	Gly	Val		
1160					1165					1170						
gct	ctg	cgt	gag	cg	ctg	tac	gag	g	ctg	gag	gtg	aag	aac	gcc		4093
Ala	Leu	Arg	Glu	Arg	Leu	Tyr	Glu	Ala	Leu	Glu	Val	Lys	Asn	Ala		
1175					1180					1185						
gaa	ttc	aac	gcc	cag	ggc	gtc	gaa	ctc	aac	cag	cgc	tac	acc	tcg		4138
Glu	Phe	Asn	Ala	Gln	Gly	Val	Glu	Leu	Asn	Gln	Arg	Tyr	Thr	Ser		
1190					1195					1200						
tcc	gcg	gtc	gtt	ccc	gac	ccc	gag	g	gc	gag	gaa	gtg	tgg	gtg		4183
Ser	Ala	Val	Val	Pro	Asp	Pro	Gl	Ala	Gly	Glu	Glu	Val	Trp	Val		
1205					1210					1215						
cgc	gat	cgt	gag	ctg	tac	ctg	cag	gcc	acc	acc	cgg	ccg	ggc	g		4228
Arg	Asp	Arg	Glu	Leu	Tyr	Leu	Gln	Ala	Thr	Thr	Arg	Pro	Gly	Ala		
1220					1225					1230						
aag	ctg	ccg	cat	g	tg	ctg	gtc	ggc	ggc	gac	gga	acc	ccg	atc		4273
Lys	Leu	Pro	His	Ala	Trp	Leu	Val	Gly	Ala	Asp	Gly	Thr	Arg	Ile		
1235					1240					1245						
tcc	acc	ctc	gac	gtc	acc	ggc	aag	g	ga	atg	acc	ctg	ctg	acc		4318
Ser	Thr	Leu	Asp	Val	Thr	Gly	Lys	Gly	Met	Met	Thr	Leu	Leu	Thr		
1250					1255					1260						
gga	ctc	ggc	ggc	cag	gca	tgg	aag	cgt	gcc	gcc	gcc	aaa	ctc	gac		4363
Gly	Leu	Gly	Gly	Gln	Ala	Trp	Lys	Arg	Ala	Ala	Ala	Lys	Leu	Asp		
1265					1270					1275						

ctg	ccg	tcc	ctg	cgg	acc	gtc	gtt	gtc	ggc	gaa	ccc	ggc	acc	atc	4408			
Leu	Pro	Phe	Leu	Arg	Thr	Val	Val	Val	Gly	Glu	Pro	Gly	Thr	Ile				
1280															1290			
gac	cct	tac	gga	tac	tgg	cgg	cg	gtc	cgc	gac	atc	gac	gag	gcc	4453			
Asp	Pro	Tyr	Gly	Tyr	Trp	Arg	Arg	Val	Arg	Asp	Ile	Asp	Glu	Ala				
1295															1305			
ggc	gcc	ctg	ctc	gtg	cgg	ccc	gac	ggc	tac	gtc	gcg	tgg	cga	cac	4498			
Gly	Ala	Leu	Leu	Val	Arg	Pro	Asp	Gly	Tyr	Val	Ala	Trp	Arg	His				
1310															1320			
agt	gct	ccg	gtc	tgg	gac	gac	acc	gaa	gcg	ctc	acc	agc	ctc	gag	4543			
Ser	Ala	Pro	Val	Trp	Asp	Asp	Thr	Glu	Ala	Leu	Thr	Ser	Leu	Glu				
1325															1335			
aac	gct	ctc	acc	gcg	gtc	ctc	gac	cac	tcg	gcc	agc	gac	aac	ggg	4588			
Asn	Ala	Leu	Thr	Ala	Val	Leu	Asp	His	Ser	Ala	Ser	Asp	Asn	Gly				
1340															1350			
aac	ccg	agc	ggc	aca	aac	gag	ccg	cag	tac	agc	acc	ccg	gcc	gtg	4633			
Asn	Pro	Ser	Gly	Thr	Asn	Glu	Pro	Gln	Tyr	Ser	Thr	Arg	Ala	Val				
1355															1365			
ccg	atc	gtc	gtt	ccg	cac	gtt	acc	gcc	gag	gat	gca	gca	cca	gct	4678			
Pro	Ile	Val	Val	Pro	His	Val	Thr	Ala	Glu	Asp	Ala	Ala	Pro	Ala				
1370															1380			
tcc	gcc	acc	cgc	acc	acc	aca	gtc	gag	gga	gag	aac	cga	tga		4720			
Ser	Ala	Thr	Arg	Thr	Thr	Thr	Val	Glu	Gly	Glu	Asn	Arg						
1385															1395			
cccggtcctta	caccagcg	tc	tgggacgacc	tgaaccagg	tg	cgagttc	agc	caggatt	ca	tc					4780			
tccaggccgg	ccc	ctt	acc	ccg	acc	tgc	ac	gccc	gg	cgactc	gtc	a	gccc	acgc	4840			
tgatcctgct	gcac	ggc	atc	acc	ggc	cc	agg	cg	ta	cgt	gc	ca	at	ctgc	gtc	4900		
attccgagca	ctt	caac	gtc	tgg	caat	cg	actt	cat	cg	cc	ac	gg	gt	atc	gac	4960		
ccgaccaccc	gct	c	gag	atc	acta	tc	gac	ca	cgt	gt	tc	gac	tt	ctgg	ac	5020		
tcggcgtcga	gaagg	cc	ctcg	ttt	ccgggg	ag	tct	tc	gg	tt	gg	tc	acc	ccc	agt	5080		
tcgcgcacga	ccat	ccc	gag	aag	gtc	acc	gg	atc	gt	g	ca	ac	acc	atg	ggc	ggcacca	5140	
tggccaaccc	tc	agg	gtat	g	a	ac	gt	ct	c	t	at	ac	cc	t	tc	g	5200	
cgagctgg	ac	gc	gt	caa	aa	ca	ac	gc	cc	at	gg	tc	at	at	gg	atc	5260	
ccgacgac	ct	at	cc	gc	acc	tc	cc	agg	cc	at	gg	at	gg	cc	tc	at	5320	
gcgagatgaa	ca	tgg	ca	ctg	c	ag	gg	ac	cc	aa	gc	gg	aa	at	cc	gg	ac	5380
ccactctcaa	cg	gcat	ca	cg	gt	g	cc	cc	gc	ga	tc	ac	cc	tc	cg	at	5440	
gtccgg	tc	ga	ag	cc	aa	cg	ca	cc	at	cc	cc	at	cc	aa	gt	cc	at	5500

tggagaactg	tggccactgg	ccccagtagc	aggaccggga	gaccttcaac	aagctgcata	5560
tggacttcct	cctcggtcgc	agctgacaca	gaccccgccc	ggtgccgcca	accctgcaa	5620
cccgccggc	accggccgga	tctcaattac	ccgacctatt	gcgctctcg	ccggacccccc	5680
ggagagaaaag	cggcgaagca	gcagcaagga	gaccgcccgc	atg cct gta	gcg ctg	5735
				Met Pro Val	Ala Leu	
				1400		
tgc gcg atg	tcg cac tcc ccc	ctg atg	gga cgc aac	gac ccc	gaa gaa	5780
Cys Ala Met	Ser His Ser Pro	Leu Met	Gly Arg Asn	Asp Pro	Glu Glu	
1405	1410	1415				
cag gaa gtc	atc gac gcc gtc	gac gcc	gca ttc gac	cac gcg	cgc cgc	5825
Gln Glu Val	Ile Asp Ala Val	Asp Asp	Ala Ala Phe	Asp His	Ala Arg	
1420	1425	1430				
cggttcgtc	gcc gac ttc gcc	ccc gat	ctc atc gtc	atc ttc	gcc gcc	5870
Arg Phe Val	Ala Asp Phe Ala	Pro Pro	Asp Leu Ile	Val Ile	Phe Ala	
1435	1440	1445				
ccc gac cac	tac aac ggc gtc	ttc tac	gac ctg ctg	ccg ccg	ttc ttc	5915
Pro Asp His	Tyr Asn Gly Val	Phe	Tyr Asp Leu	Leu Pro	Pro Phe	
1450	1455	1460				
tgt atc ggt	gcc gcc gcg cag	tcc gtc	ggc gac tac	ggc acc	gaa gaa	5960
Cys Ile Gly	Ala Ala Ala Gln	Ser Val	Gly Asp Tyr	Gly Thr	Glu Glu	
1465	1470	1475				
gcc ggc cct	ctc gac gtc gac	cgt gac	gcc gcc tac	gca gtc	gcc gcc	6005
Ala Gly Pro	Leu Asp Val Asp	Arg	Asp Ala Ala	Tyr Ala	Val Ala	
1480	1485	1490				
cgc gac gtc	ctc gac agc ggc	atc gac	gtc gca ttc	tcc tcc	gaa cgc	6050
Arg Asp Val	Leu Asp Ser Gly	Ile Ile	Asp Val Ala	Phe Ser	Glu Arg	
1495	1500	1505				
atg cac gtc	gac cac gga ttc	gcc gaa	gca ctc caa	ttt ctg	gtc gtc	6095
Met His Val	Asp His Gly Phe	Ala Ala	Gln Ala Leu	Gln Leu	Leu Val	
1510	1515	1520				
gga tcg atc	acc gcc gtg ccg	acc acc	gtg ccg atc	ttc atc	aat tcg	6140
Gly Ser Ile	Thr Ala Val Pro	Thr	Val Pro Ile	Phe Ile	Asn Ser	
1525	1530	1535				
gtc gcc gaa	ccg ctc ggc ccg	gtc agc	cggtgtt	ccg ctg	ctc ggc	6185
Val Ala Glu	Pro Leu Gly Pro	Val	Ser Arg Val	Arg Leu	Leu Gly	
1540	1545	1550				
gag gcg gtc	ggg cggttcc	gcc gct	gac aag	cgt gtg	ctg ctg	6230
Glu Ala Val	Gly Arg Ala Ala	Ala	Lys Leu Asp	Lys Arg	Val Leu	
1555	1560	1565				

tcc gtc gga	tcc ggc ggc ctg tcc	cac gac ccg ccg gtc	ccg cag	6275
Phe Val Gly	Ser Gly Gly Leu Ser	His Asp Pro Pro Val	Pro Gln	
1570	1575	1580		
tcc gcc acc	gcg cca gag gaa gtg	cgc gag cgg ttg atc	gac ggc	6320
Phe Ala Thr	Ala Pro Glu Glu Val	Arg Glu Arg Leu Ile	Asp Gly	
1585	1590	1595		
cgc aat ccc	agt gcc gcc gaa cgt	gat gcc cgc gaa cag	cgc gtc	6365
Arg Asn Pro	Ser Ala Ala Glu Arg	Asp Ala Arg Glu Gln	Arg Val	
1600	1605	1610		
atc acc gcc	ggg cg ^g gac ttc gcc	gcc ggc acc gcc gcc	atc cag	6410
Ile Thr Ala	Gly Arg Asp Phe Ala	Ala Gly Thr Ala Ala	Ile Gln	
1615	1620	1625		
cca ctg aac	ccc gaa tgg gac cg ^g	cac ctg ctc gac gtc	ctc gcc	6455
Pro Leu Asn	Pro Glu Trp Asp Arg	His Leu Leu Asp Val	Leu Ala	
1630	1635	1640		
tcc ggc gac	ctc gag cag atc gac	g ^c g tgg acc aac gac	tgg ttc	6500
Ser Gly Asp	Leu Glu Gln Ile Asp	Ala Trp Thr Asn Asp	Trp Phe	
1645	1650	1655		
gtc gaa cag	gcc gga cac tcc tcc	cac gaa gtg cgc acc	tgg atc	6545
Val Glu Gln	Ala Gly His Ser Ser	His Glu Val Arg Thr	Trp Ile	
1660	1665	1670		
gcc gcg tac	g ^c g gca atg agc gcc	gcc ggg aag tac cgc	gtc acc	6590
Ala Ala Tyr	Ala Ala Met Ser Ala	Ala Gly Lys Tyr Arg	Val Thr	
1675	1680	1685		
tcg acc ttc	tac cgc gaa atc cac	gag tgg ata gca gga	ttc ggg	6635
Ser Thr Phe	Tyr Arg Glu Ile His	Glu Trp Ile Ala Gly	Phe Gly	
1690	1695	1700		
att act acc	gcc gtc gcc gtc gac	gaa tag accccgcccc	tcccgcccc	6685
Ile Thr Thr	Ala Val Ala Val Asp	Glu		
1705	1710			
cagtcggcaac	gaagggtggc cccggatgac	ctccgtccgc ccgtgctcgc	cgtcggtgaa	6745
cgcgggctgg	tcggtgggca ggaagacctc	atcgccgaca tcgcccctcga	cctcgcagct	6805
cgtcagtagg	aatgcgcacg ggccgacgag	tcgcgcttgtt caccggggcc	agccgcggca	6865
tcggggcggc	catcgagat gcggtgccg	cctccggtgc cgccgttaatc	gtccactacg	6925
gatccgatcg	gacggccgccc gctcggtgt	cgacggcatac acggctgccc	ggggcctcgc	6985
ggctcggtc	caggccgacc tgtccgacc	cgaggggcct gaagagctga	tgcggagtt	7045
cgactccgcg	ctcgacggtc tcgggctcga	ccgagggctc gacatcctcg	tcaacaacgc	7105
cggaatcagt	cggcgccggag cgctcgagcg	cgtcaactgtc gaggatttcg	accgtctggt	7165

cgcactcaac cagcgcgccc	cgttcttcgt gactcggcat	gccctgcccc	ggatgcacga	7225	
cggcggtcgc atcgtcaaca	tttcctccgg atccgcccgc	tacgcccagac	ccgacgtcat	7285	
cagctacgcc atgaccaagg	ggcgatcga ggtgctcacc	cgcgcctcg	ccgttagacgt	7345	
cggcgaacga ggcattcacccg	ccaacgcccgt	ggcgccggcc	gcgctcgata	ccgacatgaa	7405
cgcgcactgg ctgcggtg	acgaccatgc	ccgcaccacc	gccgcgtcca	ccactgcact	7465
gcgaaaactc gccaccgcgg	aggacatcgc	cgcgatcgtg	gccttcctcg	tcagcgcgc	7525
cgcgggtgcg atcaccgggc	aggtcatcga	cgccaccaac	ggcaaccggc	tctaaccaga	7585
acttaccggg tccc				7599	

<210> 2
<211> 246
<212> PRT
<213> Rhodococcus sp.

<400> 2

Met Thr Thr Thr Asp Thr Gly Pro Lys	Pro Gly Ser Glu Ala Ala Ala		
1	5	10	15

Leu Leu Ala Asn Val Arg Thr Ser Gly Ala Arg Leu Ser Ser Ala Leu		
20	25	30

Tyr Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg Tyr Ala Ala Gly		
35	40	45

Glu Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe Gly Val Ser Lys		
50	55	60

Gln Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser Asp Lys Leu Val			
65	70	75	80

His Ile Val Pro Gln Val Gly Cys Glu Val Val Ser Tyr Ala Pro Arg		
85	90	95

Glu Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe Glu Gly Thr Ile		
100	105	110

Ala Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln Leu Leu Glu Leu		
115	120	125

Asp Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp Pro
130 135 140

Val Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His Ala
145 150 155 160

Ala Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser Gln
165 170 175

Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile Thr
180 185 190

Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His Glu
195 200 205

Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Ala Arg Glu Ala
210 215 220

Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser
225 230 235 240

Asn Ala Gln Leu Pro Ser
245

<210> 3
<211> 514
<212> PRT
<213> Rhodococcus sp.

<400> 3

Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser Arg Thr Ser Pro
1 5 10 15

Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg Ile Val Leu Arg
20 25 30

Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser Pro Thr Val Ser
35 40 45

Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu Arg Val Ala Met
50 55 60

Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp Phe Phe Ile Tyr
65 70 75 80

Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe Phe Pro Asp Val
85 90 95

Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr Phe Ser Val Gly
100 105 110

Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly His Phe Gly Asp
115 120 125

Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu Val Gly Met Gly
130 135 140

Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr Ala Gln Ile Gly
145 150 155 160

Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu Val Gln Gly Phe
165 170 175

Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met Ala Val Glu His
180 185 190

Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe Ser Gln Met Gly
195 200 205

Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe Phe Ala Val Ser
210 215 220

Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp Arg Leu Pro Phe
225 230 235 240

Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe Ile Arg Leu Ser
245 250 255

Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala Gln Ser Ala Val
260 265 270

Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His Trp Lys Glu Ile
275 280 285

Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val Phe Ala Tyr Ile
290 295 300

Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val Ala Gly Ile Ser
 305 310 315 320

Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly Ile Val Ala Val
 325 330 335

Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr Phe Gly Arg Lys
 340 345 350

Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val Val Ile Ala Pro
 355 360 365

Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu Phe Met Ala Ala
 370 375 380

Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala Ala Gly Val Thr
 385 390 395 400

Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val Arg Tyr Ser Gly
 405 410 415

Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly Ser Ala Phe Ala
 420 425 430

Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn Thr Ser Asn Ser
 435 440 445

Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser Ile Val Ser Val
 450 455 460

Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala Ala Ser Gln Leu
 465 470 475 480

Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro Asp Thr Glu Thr
 485 490 495

Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser Leu Arg Val Leu
 500 505 510

Asp Lys

<210> 4
<211> 637
<212> PRT
<213> Rhodococcus sp.

<400> 4

Val Met Thr Asp Met Ser Asp His Asp Arg Thr Ser Tyr Asp Thr Asp
1 5 10 15

Val Val Ile Val Gly Leu Gly Pro Ala Gly Gly Thr Ala Ala Leu Ala
20 25 30

Leu Ala Ser Tyr Gly Ile Arg Val His Ala Val Ser Met Phe Pro Trp
35 40 45

Val Ala Asn Ser Pro Arg Ala His Ile Thr Asn Gln Arg Ala Val Glu
50 55 60

Val Leu Arg Asp Leu Gly Val Glu Asp Glu Ala Arg Asn Tyr Ala Thr
65 70 75 80

Pro Trp Asp Gln Met Gly Asp Thr Leu Phe Thr Thr Ser Leu Ala Gly
85 90 95

Glu Glu Ile Val Arg Met Gln Thr Trp Gly Thr Gly Asp Ile Arg Tyr
100 105 110

Gly Asp Tyr Leu Ser Gly Ser Pro Cys Thr Met Leu Asp Ile Pro Gln
115 120 125

Pro Leu Met Glu Pro Val Leu Ile Lys Asn Ala Ala Glu Arg Gly Ala
130 135 140

Val Ile Ser Phe Asn Thr Glu Tyr Leu Asp His Ala Gln Asp Glu Asp
145 150 155 160

Gly Val Thr Val Arg Phe Arg Asp Val Arg Ser Gly Thr Val Phe Thr
165 170 175

Gln Arg Ala Arg Phe Leu Leu Gly Phe Asp Gly Ala Arg Ser Lys Ile
180 185 190

Ala Glu Gln Ile Gly Leu Pro Phe Glu Gly Glu Leu Ala Arg Ala Gly
195 200 205

Thr Ala Tyr Ile Leu Phe Asn Ala Asp Leu Ser Lys Tyr Val Ala His
210 215 220

Arg Pro Ser Ile Leu His Trp Ile Val Asn Ser Lys Ala Gly Phe Gly
225 230 235 240

Glu Ile Gly Met Gly Leu Leu Arg Ala Ile Arg Pro Trp Asp Gln Trp
245 250 255

Ile Ala Gly Trp Gly Phe Asp Met Ala Asn Gly Glu Pro Asp Val Ser
260 265 270

Asp Asp Val Val Leu Glu Gln Ile Arg Thr Leu Val Gly Asp Pro His
275 280 285

Leu Asp Val Glu Ile Val Ser Arg Ser Phe Trp Tyr Val Asn Arg Gln
290 295 300

Trp Ala Glu His Tyr Gln Ser Gly Arg Val Phe Cys Gly Gly Asp Ala
305 310 315 320

Val His Arg His Pro Pro Ser Ser Gly Leu Gly Ser Asn Thr Ser Met
325 330 335

Gln Asp Ala Phe Asn Leu Ala Trp Lys Ile Ala Phe Val Val Lys Gly
340 345 350

Tyr Ala Gly Pro Gly Leu Leu Glu Ser Tyr Ser Pro Glu Arg Val Pro
355 360 365

Val Gly Lys Gln Ile Val Ala Arg Ala Asn Gln Ser Arg Lys Asp Tyr
370 375 380

Ala Gly Leu Arg Glu Trp Phe Asp His Glu Ser Asp Asp Pro Val Ala
385 390 395 400

Ala Gly Leu Ala Lys Leu Lys Glu Pro Ser Ser Glu Gly Val Ala Leu
405 410 415

Arg Glu Arg Leu Tyr Glu Ala Leu Glu Val Lys Asn Ala Glu Phe Asn
420 425 430

Ala Gln Gly Val Glu Leu Asn Gln Arg Tyr Thr Ser Ser Ala Val Val
435 440 445

Pro Asp Pro Glu Ala Gly Glu Glu Val Trp Val Arg Asp Arg Glu Leu
450 455 460

Tyr Leu Gln Ala Thr Thr Arg Pro Gly Ala Lys Leu Pro His Ala Trp
465 470 475 480

Leu Val Gly Ala Asp Gly Thr Arg Ile Ser Thr Leu Asp Val Thr Gly
485 490 495

Lys Gly Met Met Thr Leu Leu Thr Gly Leu Gly Gly Gln Ala Trp Lys
500 505 510

Arg Ala Ala Ala Lys Leu Asp Leu Pro Phe Leu Arg Thr Val Val Val
515 520 525

Gly Glu Pro Gly Thr Ile Asp Pro Tyr Gly Tyr Trp Arg Arg Val Arg
530 535 540

Asp Ile Asp Glu Ala Gly Ala Leu Leu Val Arg Pro Asp Gly Tyr Val
545 550 555 560

Ala Trp Arg His Ser Ala Pro Val Trp Asp Asp Thr Glu Ala Leu Thr
565 570 575

Ser Leu Glu Asn Ala Leu Thr Ala Val Leu Asp His Ser Ala Ser Asp
580 585 590

Asn Gly Asn Pro Ser Gly Thr Asn Glu Pro Gln Tyr Ser Thr Arg Ala
595 600 605

Val Pro Ile Val Val Pro His Val Thr Ala Glu Asp Ala Ala Pro Ala
610 615 620

Ser Ala Thr Arg Thr Thr Val Glu Gly Glu Asn Arg
625 630 635

<210> 5
<211> 314
<212> PRT
<213> Rhodococcus sp.

<400> 5

Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu Met Gly Arg
1 5 10 15

Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe Asp
20 25 30

His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val Ile
35 40 45

Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro Pro
50 55 60

Phe Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr Glu
65 70 75 80

Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala Arg
85 90 95

Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg Met His
100 105 110

Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val Gly Ser Ile
115 120 125

Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val Ala Glu Pro
130 135 140

Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala Val Gly Arg
145 150 155 160

Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly Ser Gly Gly
165 170 175

Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala Pro Glu Glu
180 185 190

Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala Ala Glu Arg
195 200 205

Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp Phe Ala Ala
210 215 220

Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp Arg His Leu
225 230 235 240

Leu Asp Val Leu Ala Ser Gly Asp Leu Glu Gln Ile Asp Ala Trp Thr
245 250 255

Asn Asp Trp Phe Val Glu Gln Ala Gly His Ser Ser His Glu Val Arg
260 265 270

Thr Trp Ile Ala Ala Tyr Ala Ala Met Ser Ala Ala Gly Lys Tyr Arg
275 280 285

Val Thr Ser Thr Phe Tyr Arg Glu Ile His Glu Trp Ile Ala Gly Phe
290 295 300

Gly Ile Thr Thr Ala Val Ala Val Asp Glu
305 310

<210> 6
<211> 289
<212> PRT
<213> Rhodococcus sp.

<400> 6

Met Thr Arg Pro Tyr Thr Ser Val Trp Asp Asp Leu Asn Gln Val Glu
1 5 10 15

Phe Ser Gln Gly Phe Ile Gln Ala Gly Pro Tyr Arg Thr Arg Tyr Leu
20 25 30

His Ala Gly Asp Ser Ser Lys Pro Thr Leu Ile Leu Leu His Gly Ile
35 40 45

Thr Gly His Ala Glu Ala Tyr Val Arg Asn Leu Arg Ser His Ser Glu
50 55 60

His Phe Asn Val Trp Ala Ile Asp Phe Ile Gly His Gly Tyr Ser Thr
65 70 75 80

Lys Pro Asp His Pro Leu Glu Ile Lys His Tyr Ile Asp His Val Leu
85 90 95

Gln Leu Leu Asp Ala Ile Gly Val Glu Lys Ala Ser Phe Ser Gly Glu
100 105 110

Ser Leu Gly Gly Trp Val Thr Ala Gln Phe Ala His Asp His Pro Glu
115 120 125

Lys Val Asp Arg Ile Val Leu Asn Thr Met Gly Gly Thr Met Ala Asn
130 135 140

Pro Gln Val Met Glu Arg Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys
145 150 155 160

Asp Pro Ser Trp Glu Arg Val Lys Ala Arg Leu Glu Trp Leu Met Ala
165 170 175

Asp Pro Thr Met Val Thr Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile
180 185 190

Phe Gln Gln Pro Asp Trp Leu Lys Ala Cys Glu Met Asn Met Ala Leu
195 200 205

Gln Asp Leu Glu Thr Arg Lys Arg Asn Met Ile Thr Asp Ala Thr Leu
210 215 220

Asn Gly Ile Thr Val Pro Ala Met Val Leu Trp Thr Thr Lys Asp Pro
225 230 235 240

Ser Gly Pro Val Asp Glu Ala Lys Arg Ile Ala Ser His Ile Pro Gly
245 250 255

Ala Lys Leu Ala Ile Met Glu Asn Cys Gly His Trp Pro Gln Tyr Glu
260 265 270

Asp Pro Glu Thr Phe Asn Lys Leu His Leu Asp Phe Leu Leu Gly Arg
275 280 285

Ser

```

<210>
<211>
<212>
<213>

<400> 7

000

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> OHPR3

<400> 8
atcgaattcg gatccatgac caccacc                                27

<210> 9
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> OHPR4

<400> 9
atcgcggccg ctctagacta actgcaggc gccaaagctcg gcag                                44

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> C11

<400> 10
atcgaattcg gatccacgag agag                                24

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> C12

<400> 11
atccggccgc gctctagagt acgcaagct                                29

```

```

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> op1

<400> 12
atcctcgaga ccccgataacc 20

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> op2

<400> 13
atcgtcgacc gctaccc 17

<210> 14
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> CaMVop2

<400> 14
tccactgacg taagggatga cgcacaaatcc cactatcctt cgcaagaccc 50

<210> 15
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> CaMVop3

<400> 15
atgcttagacg tctagttcag acgctactta tatagaggaa gggcttgcg 50

<210> 16
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> CaMVop4

```

<400> 16		
cgtctagcat tctagttgag gaagttcatt tcatttggag aggac		45
<210> 17		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> CaMVopF1		
<400> 17		
atcgatatact ccactgacgt aag		23
<210> 18		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> CaMVopR1		
<400> 18		
gatggatccg tcctctccaa atga		24
<210> 19		
<211> 470		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Chimeric promoter		
<400> 19		
catgcctgca ggtcaacatg gtggagcacg acactctcgt ctactccaag aatatcaaag		60
atacagtctc agaagaccag aggctattg agactttca acaaaggta atatcggaa		120
acctccctcg attccattgc ccagctatct gtcacttcat cgaaaggaca gtagaaaagg		180
aagatggctt ctacaaatgc catcattgcg ataaaggaaa ggctatcggt caagaatgcc		240
tctaccgaca gtggtccaa agatgtaccc ccacccacga ggaacatcgt ggaaaaagaa		300
gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg		360
gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagt agcgtctgaa		420
ctagacgtct agcattctag ttgaggaagt tcatttcatt tggagaggac		470